

SEQUENCE LISTING

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<120> METHODS FOR HIGH-TEMPERATURE HYDROLYSIS OF GALACTOSE-CONTAINING
OLIGOSACCHARIDES IN COMPLEX MIXTURES

<130> 9207.4

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<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1659

<212> DNA

<213> Thermotoga maritima

<220>

<221> CDS

<222> (1)..(1659)

<223>

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gag aaa aac ttc aca gtt gag ttc gcg gtg gag aag ata cac ctt ggc 96
Glu Lys Asn Phe Thr Val Glu Phe Ala Val Glu Lys Ile His Leu Gly
20 25 30
tgg aag atc tcc ggc agg gtg aag gga agt ccg gga agg ctt gag gtt 144
Trp Lys Ile Ser Gly Arg Val Lys Gly Ser Pro Gly Arg Leu Glu Val
35 40 45
ctt cga acg aaa gca ccg gaa aag gta ctt gtg aac aac tgg cag tcc 192
Leu Arg Thr Lys Ala Pro Glu Lys Val Leu Val Asn Asn Trp Gln Ser
50 55 60
tgg gga ccg tgc agg gtg gtc gat gcc ttt tct ttc aaa cca cct gaa 240
Trp Gly Pro Cys Arg Val Val Asp Ala Phe Ser Phe Lys Pro Pro Glu
65 70 75 80
ata gat ccg aac tgg aga tac acc gct tcg gtg gtg ccc gat gta ctt 288
Ile Asp Pro Asn Trp Arg Tyr Thr Ala Ser Val Val Pro Asp Val Leu
85 90 95

gaa	agg	aac	ctc	cag	agc	gac	tat	ttc	gtg	gct	gaa	gaa	gga	aaa	gtg	336
Glu	Arg	Asn	Leu	Gln	Ser	Asp	Tyr	Phe	Val	Ala	Glu	Glu	Gly	Lys	Val	
		100						105					110			
tac	ggg	ttt	ctg	agt	tcg	aaa	atc	gca	cat	cct	ttc	ttc	gct	gtg	gaa	384
Tyr	Gly	Phe	Leu	Ser	Ser	Lys	Ile	Ala	His	Pro	Phe	Phe	Ala	Val	Glu	
		115					120					125				
gat	ggg	gaa	ctt	gtg	gca	tac	ctc	gaa	tat	ttc	gat	gtc	gag	ttc	gac	432
Asp	Gly	Glu	Leu	Val	Ala	Tyr	Leu	Glu	Tyr	Phe	Asp	Val	Glu	Phe	Asp	
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gac	ttt	gtt	cct	ctt	gaa	cct	ctc	gtt	gta	ctc	gag	gat	ccc	aac	aca	480
Asp	Phe	Val	Pro	Leu	Glu	Pro	Leu	Val	Val	Leu	Glu	Asp	Pro	Asn	Thr	
					150					155					160	
ccc	ctt	ctt	ctg	gag	aaa	tac	gcg	gaa	ctc	gtc	gga	atg	gaa	aac	aac	528
Pro	Leu	Leu	Leu	Glu	Lys	Tyr	Ala	Glu	Leu	Val	Gly	Met	Glu	Asn	Asn	
				165					170					175		
gcg	aga	gtt	cca	aaa	cac	aca	ccc	act	gga	tgg	tgc	agc	tgg	tac	cat	576
Ala	Arg	Val	Pro	Lys	His	Thr	Pro	Thr	Gly	Trp	Cys	Ser	Trp	Tyr	His	
			180					185					190			
tac	ttc	ctt	gat	ctc	acc	tgg	gaa	gag	acc	ctc	aag	aac	ctg	aag	ctc	624
Tyr	Phe	Leu	Asp	Leu	Thr	Trp	Glu	Glu	Thr	Leu	Lys	Asn	Leu	Lys	Leu	
		195					200					205				
gcg	aag	aat	ttc	ccg	ttc	gag	gtc	ttc	cag	ata	gac	gac	gcc	tac	gaa	672
Ala	Lys	Asn	Phe	Pro	Phe	Glu	Val	Phe	Gln	Ile	Asp	Asp	Ala	Tyr	Glu	
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aag	gac	ata	ggg	gac	tgg	ctc	gtg	aca	aga	gga	gac	ttt	cca	tcg	gtg	720
Lys	Asp	Ile	Gly	Asp	Trp	Leu	Val	Thr	Arg	Gly	Asp	Phe	Pro	Ser	Val	
		225			230					235					240	
gaa	gag	atg	gca	aaa	gtt	ata	gcg	gaa	aac	ggg	ttc	atc	ccg	ggc	ata	768
Glu	Glu	Met	Ala	Lys	Val	Ile	Ala	Glu	Asn	Gly	Phe	Ile	Pro	Gly	Ile	
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tgg	acc	gcc	ccg	ttc	agt	gtt	tct	gaa	acc	tcg	gat	gta	ttc	aac	gaa	816
Trp	Thr	Ala	Pro	Phe	Ser	Val	Ser	Glu	Thr	Ser	Asp	Val	Phe	Asn	Glu	
			260					265					270			
cat	ccg	gac	tgg	gta	gtg	aag	gaa	aac	gga	gag	ccg	aag	atg	gct	tac	864
His	Pro	Asp	Trp	Val	Val	Lys	Glu	Asn	Gly	Glu	Pro	Lys	Met	Ala	Tyr	
		275					280					285				
aga	aac	tgg	aac	aaa	aag	ata	tac	gcc	ctc	gat	ctt	tcg	aaa	gat	gag	912
Arg	Asn	Trp	Asn	Lys	Lys	Ile	Tyr	Ala	Leu	Asp	Leu	Ser	Lys	Asp	Glu	
		290				295					300					

His Pro Asp Trp Val Val Lys Glu Asn Gly Glu Pro Lys Met Ala Tyr
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 Arg Asn Trp Asn Lys Lys Ile Tyr Ala Leu Asp Leu Ser Lys Asp Glu
 290 295 300
 Val Leu Asn Trp Leu Phe Asp Leu Phe Ser Ser Leu Arg Lys Met Gly
 305 310 315 320
 Tyr Arg Tyr Phe Lys Ile Asp Phe Leu Phe Ala Gly Ala Val Pro Gly
 325 330 335
 Glu Arg Lys Lys Asn Ile Thr Pro Ile Gln Ala Phe Arg Lys Gly Ile
 340 345 350
 Glu Thr Ile Arg Lys Ala Val Gly Glu Asp Ser Phe Ile Leu Gly Cys
 355 360 365
 Gly Ser Pro Leu Leu Pro Ala Val Gly Cys Val Asp Gly Met Arg Ile
 370 375 380
 Gly Pro Asp Thr Ala Pro Phe Trp Gly Glu His Ile Glu Asp Asn Gly
 385 390 395 400
 Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg Tyr Phe
 405 410 415
 Met His Asp Arg Phe Trp Leu Asn Asp Pro Asp Cys Leu Ile Leu Arg
 420 425 430
 Glu Glu Lys Thr Asp Leu Thr Gln Lys Glu Lys Glu Leu Tyr Ser Tyr
 435 440 445
 Thr Cys Gly Val Leu Asp Asn Met Ile Ile Glu Ser Asp Asp Leu Ser
 450 455 460
 Leu Val Arg Asp His Gly Lys Lys Val Leu Lys Glu Thr Leu Glu Leu
 465 470 475 480
 Leu Gly Gly Arg Pro Arg Val Gln Asn Ile Met Ser Glu Asp Leu Arg
 485 490 495
 Tyr Glu Ile Val Ser Ser Gly Thr Leu Ser Gly Asn Val Lys Ile Val
 500 505 510
 Val Asp Leu Asn Ser Arg Glu Tyr His Leu Glu Lys Glu Gly Lys Ser
 515 520 525
 Ser Leu Lys Lys Arg Val Val Lys Arg Glu Asp Gly Arg Asn Phe Tyr
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 Phe Tyr Glu Glu Gly Glu Arg Glu
 545 550